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23

-1-

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: LEUNG, David W.  
TOMPKINS, Christopher K.
- (ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Foley & Lardner  
(B) STREET: 3000 K Street, N.W., Suite 500  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/842,827  
(B) FILING DATE: 17-APR-1997  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: BENT, Stephen A.  
(B) REGISTRATION NUMBER: 29,768  
(C) REFERENCE/DOCKET NUMBER: 77319/125
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (202)672-5300  
(B) TELEFAX: (202)672-5399  
(C) TELEX: 904136

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1563 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 342..1193
- (ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 342..1193
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT 60  
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCCTAACC 120

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24  
-2-

GAGTGTTCGC	GGGGGCTGTG	AGGGGAGGGC	CCCGGGCGCC	ATTGCTGGCG	GTGGGAGCGC	180
CGCCCCGTCT	CAGCCCCCCC	TCGGCTGCTC	TCCTCCTCCG	GCTGGGAGGG	GCCGTATCTC	240
GGGGCCGTCG	CCAGCCCCCG	CCCGGGCTCG	ATAATCAAGG	GCCTCGGCCG	TCGTCCCCGA	300
CCTCATTCCA	TCGCCCTTGC	CGGGCAGCCC	GGGCAGAGAC	C ATG TTT GAC AAG		353
				Met Phe Asp Lys		
				1		
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT						401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala						
5				10	15	20
GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA CGA						449
Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg						
	25			30	35	
GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA GAA GAC						497
Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys Glu Asp						
	40			45	50	
ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA TTC AGT ATT						545
Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro Phe Ser Ile						
	55			60	65	
ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT TTG						593
Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu Leu						
	70			75	80	
CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA GCC ACT ATT TAC AAA						641
His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile Tyr Lys						
	85			90	95	100
GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT GCT AGT CAG TCC CTG ACT						689
Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser Leu Thr						
	105			110	115	
GAC ATT GCC AAG TAT TCA ATA GGC AGA CTG CGG CCT CAC TTC TTG GAT						737
Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu Asp						
	120			125	130	
GTT TGT GAT CCA GAT TGG TCA AAA ATC AAC TGC AGC GAT GGT TAC ATT						785
Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile						
	135			140	145	
GAA TAC TAC ATA TGT CGA GGG AAT GCA GAA AGA GTT AAG GAA GGC AGG						833
Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu Gly Arg						
	150			155	160	
TTG TCC TTC TAT TCA GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG						881
Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu						
	165			170	175	180
TTT GTG GCA CTT TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA						929
Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg						
	185			190	195	
CTC TTA CGC CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT						977
Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr						
	200			205	210	
GTG GGC CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG						1025
Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val						
	215			220	225	

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25  
-3

TTG ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val 230 235 240	1073
TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA AAA Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys 245 250 255 260	1121
GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG AAT Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly Asn 265 270 275	1169
CAC TAT CCG AGC AAT CAC CAG CCT TGAAAGGCAG CAGGGTGCCC AGGTGAAGCT His Tyr Pro Ser Asn His Gln Pro 280	1223
GGCCTGTTTT CTAAAGGAAA ATGATTGCCA CAAGGCAAGA GGATGCATCT TTCTTCCTGG	1283
TGTACAAGCC TTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA CTTTGTGTGT	1343
ACATAGTTAC CTTTAACTCA GTGGTTATCT AATAGCTCTA AACTCATTA AAAAACTCCA	1403
AGCCTTCCAC CAAAACAGTG CCCACCTGT ATACATTTTT ATTAAAAAAA TGTAATGCTT	1463
ATGTATAAAC ATGTATGTAA TATGCTTTCT ATGAATGATG TTTGATTTAA ATATAATACA	1523
TATTAAAATG TATGGGAGAA CCAAAAAAAAA AAAAAAAAAA	1563

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys 1 5 10 15
Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr 20 25 30
Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro 35 40 45
Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile 50 55 60
Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr 65 70 75 80
Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala 85 90 95
Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser 100 105 110
Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro 115 120 125
His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser 130 135 140

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24  
-4-

Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val  
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly  
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala  
195 200 205

Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His  
210 215 220

Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile  
225 230 235 240

Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe  
245 250 255

Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro  
260 265 270

Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 342..1196

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 342..1196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT	60
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGC ACTAACC	120
GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC	180
CGCCCGGTCT CAGCCCGCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC	240
GGGGCCGTCG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA	300
CCTCATTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG	353
Met Phe Asp Lys	
1	
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	
5 10 15 20	

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27  
-57

TCC	ATG	CCT	ATG	GCT	GTT	CTA	AAA	TTG	GGC	CAA	ATA	TAT	CCA	TTT	CAG	449
Ser	Met	Pro	Met	Ala	Val	Leu	Lys	Leu	Gly	Gln	Ile	Tyr	Pro	Phe	Gln	
				25					30					35		
AGA	GGC	TTT	TTC	TGT	AAA	GAC	AAC	AGC	ATC	AAC	TAT	CCG	TAC	CAT	GAC	497
Arg	Gly	Phe	Phe	Cys	Lys	Asp	Asn	Ser	Ile	Asn	Tyr	Pro	Tyr	His	Asp	
			40					45					50			
AGT	ACC	GCC	GCA	TCC	ACT	GTC	CTC	ATC	CTA	GTG	GGG	GTT	GGC	TTG	CCC	545
Ser	Thr	Ala	Ala	Ser	Thr	Val	Leu	Ile	Leu	Val	Gly	Val	Gly	Leu	Pro	
		55					60					65				
GTT	TCC	TCT	ATT	ATT	CTT	GGA	GAA	ACC	CTG	TCT	GTT	TAC	TGT	AAC	CTT	593
Val	Ser	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val	Tyr	Cys	Asn	Leu	
	70					75					80					
TTG	CAC	TCA	AAT	TCC	TTT	ATC	AGT	AAT	AAC	TAC	ATA	GCC	ACT	ATT	TAC	641
Leu	His	Ser	Asn	Ser	Phe	Ile	Ser	Asn	Asn	Tyr	Ile	Ala	Thr	Ile	Tyr	
	85				90					95					100	
AAA	GCC	ATT	GGA	ACC	TTT	TTA	TTT	GGT	GCA	GCT	GCT	AGT	CAG	TCC	CTG	689
Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala	Ser	Gln	Ser	Leu	
				105					110					115		
ACT	GAC	ATT	GCC	AAG	TAT	TCA	ATA	GGC	AGA	CTG	CGG	CCT	CAC	TTC	TTG	737
Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	Pro	His	Phe	Leu	
			120					125					130			
GAT	GTT	TGT	GAT	CCA	GAT	TGG	TCA	AAA	ATC	AAC	TGC	AGC	GAT	GGT	TAC	785
Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser	Asp	Gly	Tyr	
		135				140						145				
ATT	GAA	TAC	TAC	ATA	TGT	CGA	GGG	AAT	GCA	GAA	AGA	GTT	AAG	GAA	GGC	833
Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg	Val	Lys	Glu	Gly	
	150					155					160					
AGG	TTG	TCC	TTC	TAT	TCA	GGC	CAC	TCT	TCG	TTT	TCC	ATG	TAC	TGC	ATG	881
Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	Met	Tyr	Cys	Met	
	165				170					175					180	
CTG	TTT	GTG	GCA	CTT	TAT	CTT	CAA	GCC	AGG	ATG	AAG	GGA	GAC	TGG	GCA	929
Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	Gly	Asp	Trp	Ala	
				185					190					195		
AGA	CTC	TTA	CGC	CCC	ACA	CTG	CAA	TTT	GGT	CTT	GTT	GCC	GTA	TCC	ATT	977
Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val	Ala	Val	Ser	Ile	
			200					205					210			
TAT	GTG	GGC	CTT	TCT	CGA	GTT	TCT	GAT	TAT	AAA	CAC	CAC	TGG	AGC	GAT	1025
Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	His	Trp	Ser	Asp	
		215					220					225				
GTG	TTG	ACT	GGA	CTC	ATT	CAG	GGA	GCT	CTG	GTT	GCA	ATA	TTA	GTT	GCT	1073
Val	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	Val	Ala	Ile	Leu	Val	Ala	
	230					235					240					
GTA	TAT	GTA	TCG	GAT	TTC	TTC	AAA	GAA	AGA	ACT	TCT	TTT	AAA	GAA	AGA	1121
Val	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr	Ser	Phe	Lys	Glu	Arg	
	245				250					255				260		
AAA	GAG	GAG	GAC	TCT	CAT	ACA	ACT	CTG	CAT	GAA	ACA	CCA	ACA	ACT	GGG	1169
Lys	Glu	Glu	Asp	Ser	His	Thr	Thr	Leu	His	Glu	Thr	Pro	Thr	Thr	Gly	
				265					270					275		
AAT	CAC	TAT	CCG	AGC	AAT	CAC	CAG	CCT	TGAAAGGCAG	CAGGGTGCCC						1216
Asn	His	Tyr	Pro	Ser	Asn	His	Gln	Pro								
			280					285								

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28

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AGGTGAAGCT GGCCTGTTTT CTAAAGGAAA ATGATTGCCA CAAGGCAAGA GGATGCATCT 1276
TTCTTCCTGG TGTACAAGCC TTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA 1336
CTTTGTGTGT ACATAGTTAC CTTTAACTCA GTGGTTATCT AATAGCTCTA AACTCATTA 1396
AAAAACTCCA AGCCTTCCAC CAAAACAGTG CCCCACCTGT ATACATTTTT ATTAAAAAAA 1456
TGTAATGCTT ATGTATAAAC ATGTATGTAA TATGCTTTCT ATGAATGATG TTTGATTTAA 1516
ATATAATACA TATTAAATG TATGGGAGAA CCAAAAAAAA AAAAAAAA 1566
  
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys
 1           5           10           15
Val Leu Leu Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile
          20           25           30
Tyr Pro Phe Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr
          35           40           45
Pro Tyr His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly
          50           55           60
Val Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val
          65           70           75           80
Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Ser Asn Asn Tyr Ile
          85           90           95
Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala
          100          105          110
Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg
          115          120          125
Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys
          130          135          140
Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg
          145          150          155          160
Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser
          165          170          175
Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys
          180          185          190
Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val
          195          200          205
Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His
          210          215          220
  
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20250422 14:22:40

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29  
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His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala
225                230                235                240

Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser
                245                250                255

Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr
                260                265                270

Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
                275                280                285

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 294..1226

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 294..1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GGCGCAGCTC TGCAAAAGTT TCTGCTCGGG ATCTGGCTCT CTTCCTTGG GACTTTAGAA      60
CGATTTAGGG TTGACAGAGG AAAGCAGAGG CGCGCAGGAG GAGCAGAAAA CACCACCTTC      120
TGCAGTTGGA GGCAGGCAGC CCCGGCTGCA CTCTAGCCGC CGCGCCCGGA GCCGGGGCCG      180
ACCCGCCACT ATCCGCAGCA GCCTCGGCCA GGAGGCGACC CGGGCGCCTG GGTGTGTGGC      240
TGCTGTTGCG GGACGTCTTC GCGGGGCGGG AGGCTCGCGC CGCAGCCAGC GCC ATG      296
                                   Met
                                   1

CAA AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC      344
Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly
                    5                10                15

GGC AGC CCG GCG CTC AAC AAC AAC CCG AGG AGG AGC GGC AGC AAG CGG      392
Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys Arg
                20                25                30

GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG GGC CTC      440
Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly Leu
                35                40                45

CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC CAC CGA GGG      488
Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg Gly
                50                55                60                65

TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG AAA ACT GGT GAG      536
Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly Glu
                70                75                80

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30  
-8-

[illegible]



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31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn  
1 5 10 15  
Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys  
20 25 30  
Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly  
35 40 45  
Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg  
50 55 60  
Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly  
65 70 75 80  
Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala  
85 90 95  
Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys  
100 105 110  
Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys  
115 120 125  
Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr  
130 135 140  
Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser  
145 150 155 160  
Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile  
165 170 175  
Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg  
180 185 190  
Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu  
195 200 205  
Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg  
210 215 220  
Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr  
225 230 235 240  
Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val  
245 250 255  
Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe  
260 265 270  
Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala  
275 280 285  
Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg  
290 295 300

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32  
-10-

Asn Asn His His Asn Met Met  
305 310

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..833

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 4..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC ATG CAG CGG AGG TGG GTC TTC GTG CTG CTC GAC GTG CTG TGC TTA 48  
Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu  
1 5 10 15

CTG GTC GCC TCC CTG CCC TTC GCT ATC CTG ACG CTG GTG AAC GCC CCG 96  
Leu Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro  
20 25 30

TAC AAG CGA GGA TTT TAC TGC GGG GAT GAC TCC ATC CGG TAC CCC TAC 144  
Tyr Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr  
35 40 45

CGT CCA GAT ACC ATC ACC CAC GGG CTC ATG GCT GGG GTC ACC ATC ACG 192  
Arg Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr  
50 55 60

GCC ACC GTC ATC CTT GTC TCG GCC GGG GAA GCC TAC CTG GTG TAC ACA 240  
Ala Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr  
65 70 75

GAC CGG CTC TAT TCT CGC TCG GAC TTC AAC AAC TAC GTG GCT GCT GTA 288  
Asp Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val  
80 85 90 95

TAC AAG GTG CTG GGG ACC TTC CTG TTT GGG GCT GCC GTG AGC CAG TCT 336  
Tyr Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser  
100 105 110

CTG ACA GAC CTG GCC AAG TAC ATG ATT GGG CGT CTG AAG CCC AAC TTC 384  
Leu Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe  
115 120 125

CTA GCC GTC TGC GAC CCC GAC TGG AGC CGG GTC AAC TGC TCG GTC TAT 432  
Leu Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr  
130 135 140

GTG CAG CTG GAG AAG GTG TGC AGG GGA AAC CCT GCT GAT GTC ACC GAG 480  
Val Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu  
145 150 155

GCC AGG TTG TCT TTC TAC TCG GGA CAC TCT TCC TTT GGG ATG TAC TGC 528  
Ala Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys  
160 165 170 175

20250424 14:40:00

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33  
-11-

ATG GTG TTC TTG GCG CTG TAT GTG CAG GCA CGA CTC TGT TGG AAG TGG	576
Met Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp	
180 185 190	
GCA CGG CTG CTG CGA CCC ACA GTC CAG TTC TTC CTG GTG GCC TTT GCC	624
Ala Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala	
195 200 205	
CTC TAC GTG GGC TAC ACC CGC GTG TCT GAT TAC AAA CAC CAC TGG AGC	672
Leu Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser	
210 215 220	
GAT GTC CTT GTT GGC CTC CTG CAG GGG GCA CTG GTG GCT GCC CTC ACT	720
Asp Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr	
225 230 235	
GTC TGC TAC ATC TCA GAC TTC TTC AAA GCC CGA CCC CCA CAG CAC TGT	768
Val Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys	
240 245 250 255	
CTG AAG GAG GAG GAG CTG GAA CGG AAG CCC AGC CTG TCA CTG ACG TTG	816
Leu Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu	
260 265 270	
ACC CTG GGG CGA GGC TG ACCACAACCA CTTATGGGAT ACCCGCACTC	863
Thr Leu Gly Arg Gly	
275	
TTCTTCCTGA GGCCGGACCC CGCCCAGGCA GGGAGCTGCT GTGAGTCCAG CTGATGCCCCA	923
CCCAGGTGGT CCCTCCAGCC TGGTTAGGCA CTGAGGGTTC TGGACGGGCT CCAGGAACCC	983
TGGGCTGATG GGAGCAGTGA GCGGTTCCGC TGCCCCCTGC CCTGCACTGG ACCAGGAGTC	1043
TGGAGATGCC TGGGTAGCCC TCAGCATTTG GAGGGGAACC TGTTCCCGTC GGTCCCCAAA	1103
TATCCCCTTC TTTTATGGG GTTAAGGAAG GGACCGAGAG ATCAGATAGT TGCTGTTTTG	1163
TAAAATGTAA TGTATATGTG GTTTTATAGTA AAATAGGGCA CCTGTTTCAC AAAAAAAAAA	1223
AAAAAAAAA	1232

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gln	Arg	Arg	Trp	Val	Phe	Val	Leu	Leu	Asp	Val	Leu	Cys	Leu	Leu
1				5				10					15		
Val	Ala	Ser	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Leu	Val	Asn	Ala	Pro	Tyr
			20					25					30		
Lys	Arg	Gly	Phe	Tyr	Cys	Gly	Asp	Asp	Ser	Ile	Arg	Tyr	Pro	Tyr	Arg
		35					40					45			
Pro	Asp	Thr	Ile	Thr	His	Gly	Leu	Met	Ala	Gly	Val	Thr	Ile	Thr	Ala
	50					55					60				

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34  
-12-

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp  
 65 70 75 80  
 Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr  
 85 90 95  
 Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu  
 100 105 110  
 Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu  
 115 120 125  
 Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val  
 130 135 140  
 Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala  
 145 150 155 160  
 Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met  
 165 170 175  
 Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala  
 180 185 190  
 Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu  
 195 200 205  
 Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp  
 210 215 220  
 Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val  
 225 230 235 240  
 Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu  
 245 250 255  
 Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr  
 260 265 270  
 Leu Gly Arg Gly  
 275

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Ile Cys  
 1 5 10 15  
 Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr  
 20 25 30  
 Pro Phe Gln Arg Gly Ile Phe Cys Asn Asp Asp Ser Ile Lys Tyr Pro  
 35 40 45  
 Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Val Ile  
 50 55 60

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35  
-13-

Pro	Phe	Cys	Ile	Ile	Val	Met	Ser	Ile	Gly	Glu	Ser	Leu	Ser	Val	Tyr	65	70	75	80
Phe	Asn	Val	Leu	His	Ser	Asn	Ser	Phe	Val	Gly	Asn	Pro	Tyr	Ile	Ala	85	90	95	
Thr	Ile	Tyr	Lys	Ala	Val	Gly	Ala	Phe	Leu	Phe	Gly	Val	Ser	Ala	Ser	100	105	110	
Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Thr	Ile	Gly	Ser	Leu	Arg	Pro	115	120	125	
His	Phe	Leu	Ala	Ile	Cys	Asn	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser	130	135	140	
Asp	Gly	Tyr	Ile	Glu	Asp	Tyr	Ile	Cys	Gln	Gly	Asn	Glu	Glu	Lys	Val	145	150	155	160
Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	Met	165	170	175	
Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	Gly	180	185	190	
Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Met	Leu	Gln	Phe	Gly	Leu	Ile	Ala	195	200	205	
Phe	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	His	210	215	220	
Trp	Ser	Asp	Val	Thr	Val	Gly	Leu	Ile	Gln	Gly	Ala	Ala	Met	Ala	Ile	225	230	235	240
Leu	Val	Ala	Leu	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Asp	Thr	His	Ser	Tyr	245	250	255	
Lys	Glu	Arg	Lys	Glu	Glu	Asp	Pro	His	Thr	Thr	Leu	His	Glu	Thr	Ala	260	265	270	
Ser	Ser	Arg	Asn	Tyr	Ser	Thr	Asn	His	Glu	Pro						275	280		

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 284 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Phe	Asp	Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys	1	5	10	15
Val	Leu	Leu	Ala	Gly	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Ser	Arg	His	Thr	20	25	30	
Pro	Phe	Gln	Arg	Gly	Val	Phe	Cys	Asn	Asp	Glu	Ser	Ile	Lys	Tyr	Pro	35	40	45	
Tyr	Lys	Glu	Asp	Thr	Ile	Pro	Tyr	Ala	Leu	Leu	Gly	Gly	Ile	Ile	Ile	50	55	60	

Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr  
65 70 75 80

Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala  
85 90 95

Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser  
100 105 110

Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro  
115 120 125

His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser  
130 135 140

Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val  
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly  
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala  
195 200 205

Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His  
210 215 220

Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile  
225 230 235 240

Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe  
245 250 255

Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro  
260 265 270

Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys  
1 5 10 15

Val Leu Leu Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile  
20 25 30

Tyr Pro Phe Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr  
35 40 45

Pro Tyr His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly  
50 55 60

37

-15-

Val Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val  
65 70 75 80

Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile  
85 90 95

Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala  
100 105 110

Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg  
115 120 125

Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys  
130 135 140

Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg  
145 150 155 160

Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser  
165 170 175

Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys  
180 185 190

Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val  
195 200 205

Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His  
210 215 220

His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala  
225 230 235 240

Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser  
245 250 255

Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr  
260 265 270

Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280 285

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn  
1 5 10 15

Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys  
20 25 30

Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly  
35 40 45

Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg  
50 55 60

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38  
-16-

Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly  
 65 70 75 80  
 Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala  
 85 90 95  
 Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys  
 100 105 110  
 Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys  
 115 120 125  
 Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr  
 130 135 140  
 Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser  
 145 150 155 160  
 Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile  
 165 170 175  
 Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg  
 180 185 190  
 Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu  
 195 200 205  
 Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg  
 210 215 220  
 Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr  
 225 230 235 240  
 Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val  
 245 250 255  
 Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe  
 260 265 270  
 Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala  
 275 280 285  
 Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg  
 290 295 300  
 Asn Asn His His Asn Met Met  
 305 310

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu  
 1 5 10 15  
 Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr  
 20 25 30

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- 40  
-18-
- (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCACGCAT GCACCATGGT AATAGC

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGTCATGCG TGAGGCTCCG GTGC

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

G TAGTTTTCA CGGTACCTGA AATGGAAG

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCATGGTAC CATGTTTGAC AAGACGCGGC

30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

a

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

47

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

24